AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application.

Listing of claims:

1. (Currently amended) A method for determining the predisposition of an individual to a physiological reaction ~~of an individual~~ to a biologically active compound, said method comprising determining the presence of a polymorphic or haplotypic variation in the ~~characterizing~~ nucleotide sequence of ~~at least one of~~ the ~~*UGT1A1, UGT1A7* and~~ *UGT1A9* gene or a part thereof of said individual, wherein the presence of ~~at least one~~ the polymorphic or haplotypic variation in said nucleotide sequence is indicative of said predisposition ~~to a physiological reaction~~.

2. (Original) The method of claim 1, wherein said predisposition is a hereditary predisposition.

3. (Currently amended) The method of claim 1, wherein said predisposition is selected from the group consisting of a susceptibility, sensibility, diathesis, proneness, proclivity, tendency, sensitivity, responsiveness, resistance ~~or~~ and constitutional sickness to said physiological reaction.

4. (Original) The method of claim 1, wherein said physiological reaction is a beneficial reaction.

5. (Currently amended) The method of claim 1, wherein said physiological reaction is at least one of an adverse reaction, ~~or~~ a side effect, and response to therapy.

6. (Original) The method of claim 1, wherein said biologically active compound is a xenobiotic.

7. (Currently amended) The method of claim 6, wherein said xenobiotic is selected from the group consisting of a drug, a carcinogen ~~or~~ and a pre-carcinogen.

8. (Original) The method of claim 7, wherein said drug is an anti-cancer agent or an immunosuppressive agent.

9. (Original) The method of claim 8, wherein said anti-cancer agent is a camptothecin or an analog thereof.

10. (Currently amended) The method of claim 9, wherein said camptothecin analog is 7-ethyl-10-[4-(1-piperidino)-1-piperidino] carbonyloxy camptothecin (irinotecan, CPT-11)~~,~~ or 7-ethyl-10-hydroxycamptothecin (SN-38).

11. (Original) The method of claim 8, wherein said immunosuppressive agent is mycophenolic acid (MPA).

12. (Original) The method of claim 1, wherein said individual is a human or an animal.

13. (Currently amended) The method of claim 1, wherein said individual ~~is a patient with~~ has a cancer.

14. (Currently amended) The method of claim 13, wherein said ~~patient has a~~ cancer is at least one of colorectal cancer, ~~or~~ a solid tumor and a hematological cancer.

15. (Currently amended) The method of claim 1, wherein said determining ~~genetic sequence~~ is performed on a DNA or a RNA sample of said individual.

16. (Cancelled)

17. (Currently amended) The method of claim 16, wherein said ~~UGT1A9 variation~~ polymorphic or haplotypic variation is at least one of a $C^{-2208}T$ substitution, a $C^{-2152}T$ substitution, a $C^{-2141}T$ substitution, a $T^{-1887}G$ substitution, a $T^{-1818}C$ substitution, a $C^{-665}T$ substitution, a $T^{-440}C$ substitution, a $C^{-331}T$ substitution, a $T^{-275}A$ substitution, a $G^{-87}A$ substitution, a $G^{8}A$ missence mutation ($C^{3}Y$), and a $T^{98}C$ missence mutation ($M^{33}T$) ~~or combination thereof~~.

18. (Original) The method of claim 17, wherein said $G^{8}A$ missence mutation is associated with a decreased predisposition or susceptibility to an anti-cancer agent.

19. (Original) The method of claim 17, wherein said $G^{8}A$ missence mutation is associated with a decreased responsiveness to an immunosuppressive agent.

20. (Original) The method of claim 17, wherein said $T^{98}C$ missence mutation is associated with an increased adverse reaction to an anti-cancer agent.

21. (Currently amended) The method of claim 1, further comprising determining the presence of a ~~wherein said~~ polymorphic or haplotypic variation is a the UGT1A7 ~~variation~~gene.

22. (Currently amended) The method of claim 21, wherein said ~~UGT1A7 variation~~ polymorphic or haplotypic variation is at least one of a $G^{353}T$ missense mutation, a $T^{397}G$ missense mutation, a $C^{401}A$ missense mutation, a $G^{402}A$ missense mutations, a $G^{427}C$ missense mutation, and a $T^{632}C$ missense mutation ~~or combination thereof~~.

23. (Currently amended) The method of claim 21, further comprising determining the presence of a ~~wherein said~~ polymorphic or haplotypic variation is a the UGT1A1 ~~variation~~gene.

24. (Currently amended) The method of claim 23, wherein said ~~UGT1A1 variation~~ polymorphic or haplotypic variation is a TA_7 mutation in the TATA box.

25. (Withdrawn) An isolated nucleotide sequence comprising at least one nucleotide sequence selected from the group consisting of SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45 SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, SEQ ID NO: 52, SEQ ID NO: 53, SEQ ID NO: 54, SEQ ID NO: 55, SEQ ID NO: 56, SEQ ID NO: 57, SEQ ID NO: 58, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 61, SEQ ID NO: 62, SEQ ID NO: 63, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 66, SEQ ID NO: 67, SEQ ID NO: 68, a fragment or the complementary sequences thereof, for determining predisposition to a physiological reaction.

26. (Withdrawn) The nucleotide sequence of claim 25, wherein said sequence is an allelic variant of UGT1A1, UGT1A7 or UGT1A9.

27. (Withdrawn) An isolated amino acid sequence comprising at least one amino acid sequence selected from the group consisting of SEQ ID NO: 69, SEQ ID NO: 70, SEQ ID NO: 71 or a fragment thereof.

28. (Withdrawn) The amino acid sequence of claim 27, wherein said sequence is encoded by a nucleotide sequence comprising at least one sequence selected from the group consisting of SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, a fragment or the complementary sequences thereof.

29. (Withdrawn) The amino acid sequence of claim 27, wherein the expression of said sequence is regulated by a nucleotide sequence comprising at least one sequence selected from the group consisting of SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45 SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, SEQ ID NO: 52, SEQ ID NO: 53, SEQ ID NO: 54, SEQ ID NO: 55, SEQ ID NO: 56, SEQ ID NO: 57, SEQ ID NO: 58, SEQ ID NO: 59, a fragment or the complementary sequences thereof.